IN THE SPECIFICATION:

Please amend the paragraph beginning on page 62, line 16 as follows:

As a consequence of using the 1907*Bam*HI F ~~[SEQ ID NO: 9]~~(SEQ ID NO:9) and 1907*Pst*R ~~[SEQ ID NO:10]~~(SEQ ID NO: 10) oligonucleotides as primers in the PCR and of the subsequent cloning of the product into pQE30, the sequence of the *Petunia* E20 clone was altered around the putative initiating methionine of the encoded polypeptide. As a consequence the expected amino acids around the putative initiating methionine were changed from "M T G K T A H P" (SEQ ID NO: 48) to "M R G S H H H H H H G S T G K T A H P" (SEQ ID NO: 49).

Please amend the paragraph beginning on page 62, line 23 as follows:

According to the manufacturer, "the 6 x His-tag is much smaller than most other affinity tags and is uncharged at physiological pH. It rarely alters or contributes to protein immunogenicity, rarely interferes with protein structure or function, does not interfere with secretion, does not require removal by protease cleavage, and is compatible with denaturing buffer systems". (QIAGEN website~~, http://www.qiagen.com~~).

Please amend the paragraph beginning on page 74, line 20 as follows:

As a consequence of using the TMT5.*Bam*HI.F ~~[SEQ ID NO:13]~~(SEQ ID NO: 13) and TMT5.*Pst*I.R ~~[SEQ ID NO:14]~~(SEQ ID NO: 14) oligonucleotides as primers in the PCR and of the subsequent cloning of the product into pQE30, the sequence of the *Torenia* FMT clone was altered around the putative initiating methionine of the encoded polypeptide. As a consequence the expected amino acids around the putative initiating methionine were changed from "M K D K F Y G T"(SEQ ID NO: 50) to "M R G S H H H H H H G S K D K F Y G T"(SEQ ID NO: 51).

Please amend the paragraph beginning on page 100, line 18 as follows:

The CODEHOP (COnsensus-DEgenerate Hybrid Oligonucleotide Primers) strategy (Rose *et al.*, *Nucl Acids Res, 26*: 1628-1635, 1998) ~~(outlined at http://blocks.fhcrc.org/codehop.thml)~~ was used. The CODEHOP program designs a pool of primers containing all possible 11– or 12-mers for a 3' degenerate "core" region and having the most probable nucleotide predicted for each position in a 5' non-degenerate "clamp" region (Table 24).

Please delete the Sequence Listing of record and substitute therefor with the enclosed Sequence Listing.